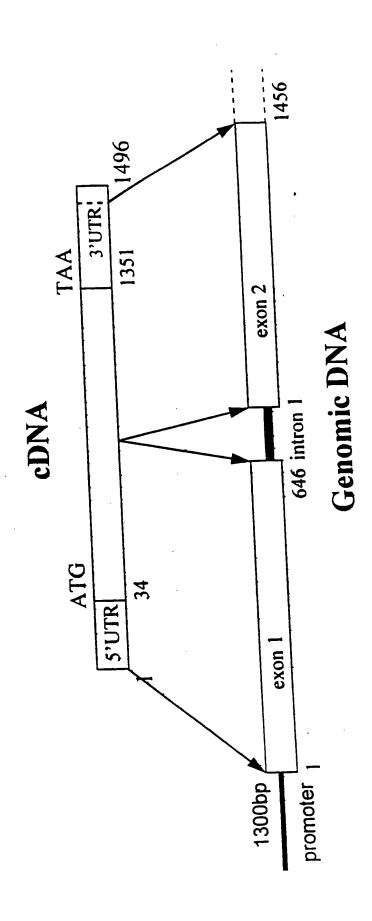
FIGURE 1



		10	20	30	40	50	
MOUSE-X1.DNA	1	ATGAGGCTTC	CTGGTTGGTT				5
HUMAN-X1.DNA	. 1	ATGAAGCTGG	CTAACTGGTA	CTGGCTGAGC	TCAGCTGTTC	TTGCCACTTA	5
		60	70			100	J
MOUSE-X1.DNA	51	CCGAGCG	GTGGAGGAGC	ACAACCTGAC	TGAGGGGCTG	GAGGATGCCA	10
HUMAN-X1.DNA	51	CGGTTTTTTG	GTTGTGGCAA	ACAATGAAAC	AGAGGAAATT	AAAGATGAAA	10
		110	120	130	140	150	10
MOUSE-X1.DNA	101	GCGCCCAGGC	TGCCTGCCCC	GCGAGGCTGG			15
HUMAN-X1.DNA	101	GAGCAAAGGA	TGTCTGCCCA	GTGAGACTAG	AAAGCAGAGG	GAAATGCGAA	15
		160	170	180	190	200	15
MOUSE-X1.DNA	151	GGGAGCC	AGTGCCCCTT	CCAGCTCACC			. 20
HUMAN-X1.DNA		GAGGCAGGGG					20
		210	220	230	240	250	20
MOUSE-X1.DNA	201	GCTCCCGCGG	CAGCTTGGCA	GCATGGAGGA	GGTGCTCAAA		25
HUMAN-X1.DNA	201	GCTCCCGAAG	CAATTCAGCA	GGATCGAGGA	GGTGTTCAAA	GAAGTCCAAA	25
		260	270	280	290	300	
MOUSE-X1.DNA	251	CCCTCAAGGA	AGCAGTGGAC	AGTCTGAAGA	AATCCTGCCA	GGACTGTAAG	30
HUMAN-X1.DNA	251	ACCTCAAGGA	AATCGTAAAT	AGTCTAAAGA	AATCTTGCCA	AGACTGCAAG	30
	• 1	310	320	330	340	350	
MOUSE-X1.DNA	301	TTGCAGGCTG	ACGACCATCG	AGATCCCGGC	GGGAATGGAG		350
HUMAN-X1.DNA	301	CTGCAGGCTG	ATGACAACGG	AGACCCAGGC	AGAAACGGAC	TGTTGTTACC	350
	•	360	370	380	390	400	
MOUSE-X1.DNA	351	-AATGGA	GCAGAGA	CAGCCGAGGA	CAGTAGAGTC	CAGGAACTGG	400
HUMAN-X1.DNA	351	CAGTACAGGA	GCCCCGGGAG	AGGTTGGTGA	TAACAGAGTT	AGAGAATTAG	400
	į	410	420	430	440	450	
MOUSE-X1.DNA	, 401	AGAGTCAGGT	GAACAAGCTG	TCCTCAGAGC	TGAAGAATGC	AAAGGACCAG	450
HUMAN-X1.DNA	401	AGAGTGAGGT	TAACAAGCTG	TCCTCTGAGC	TAAAGAATGC	CAAAGAGGAG	450
		460	470	480	490	500	
MOUSE-X1.DNA		ATCCAGGGGC					500
HUMAN-X1.DNA	451	ATCAATGTAC	TTCATGGTCG	CCTGGAGAAG	CTGAATCTTG	TAAATATGAA	500
		510	520	530	540	550	
MOUSE-X1.DNA		CAACATTGAG					550
HUMAN-X1.DNA	501	CAACATAGAA	AATTATGTTG	ACAGCAAAGT	GGCAAATCTA	ACATTTGTTG	550
		560	570	580	590	600	
MOUSE-X1.DNA		TCAACAGTTT					600
HUMAN-X1.DNA	551	TCAATAGTTT	GGATGGCAAA	TGTTCAAAGT	GTCCCAGCCA	AGAACAAATA	606
		610	620	630	640	650	
MOUSE-X1.DNA		CAGTCACAGC		• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	650
HUMAN-X1.DNA	601	CAGTCACGTC	CAG				

		10	20	30	40	50	
MOUSE-X2.DNA	٠ 1	TTCAACATCT					50
HUMAN-X2.DNA	1			GATTGCTCTG			50
		60	70	80	90	100	30
MOUSE-X2.DNA	51	AGAAGCAGTG	GGGCCTACAG	AGTTACCCCT	GATCACAGAA	ACAGCAGCTT	100
HUMAN-X2.DNA	51	AGAAGCAGTG	AGACCTACAG	AGTTACACCT	GATCCCAAAA	ATAGTAGCTT	100
		110	120	130	140	150	
MOUSE-X2.DNA	101	TGAGGTCTAC	TGTGACATGG	AGACCATGGG	TGGAGGCTGG	ACGGTGCTGC	150
HUMAN-X2.DNA		TGAAGTTTAC					150
		160	170	180	190	200	
MOUSE-X2.DNA	151	AGGCTCGCCT	TGATGGCAGC	ACCAACTTCA	CCAGAGAGTG	GAAAGACTAC	. 200
HUMAN-X2.DNA		AGGCACGTCT					200
		210	220	230	240	250	
MOUSE-X2.DNA	201	AAAGCCGGCT	TTGGAAACCT	TGAACGAGAA	TTTTGGTTGG	GCAACGATAA	250
HUMAN-X2.DNA	201	AAAGCAGGCT	TTGGAAACCT	CAGAAGGGAA	TTTTGGCTGG	GGAACGATAA	250
		260	270	280	290	300	
MOUSE-X2.DNA		AATTCATCTT					300
HUMAN-X2.DNA	251	AATTCATCTT	CTGACCAAGA	GTAAGGAAAT	GATTCTGAGA	ATAGATCTTG	300
		310	320	330	340	350	
MOUSE-X2.DNA	301	AAGACTTTAA	TGGTCTCACA	CTTTATGCCT	TGTATGATCA	GTTTTATGTG	350
HUMAN-X2.DNA	301	AAGACTTTAA	TGGTGTCGAA	CTATATGCCT	TGTATGATCA	GTTTTATGTG	350
		360	370	380	390	400	
MOUSE-X2.DNA	351	GCTAATGAAT	TTCTCAAATA	CCGATTACAC	ATCGGTAACT	ACAATGGCAC	400
HUMAN-X2.DNA	351	GCTAATGAGT	TTCTCAAATA	TCGTTTACAC	GTTGGTAACT	ATAATGGCAC	400
		410	420	430	440	450	
MOUSE-X2.DNA		GGCAGGGGAT					450
HUMAN-X2.DNA	401	AGCTGGAGAT	GCATTACGTT	TCAACAAACA	TTACAACCAC	GATCTGAAGT	450
		460	470	480	490	500	
MOUSE-X2.DNA		TTTTCACAAC					500
HUMAN-X2.DNA	451	TTTTCACCAC		GACAATGATC	GATATCCTTC	TGGGAACTGT	500
		510	520	530	540	550	
MOUSE-X2.DNA		GGGCTCTATT					550
HUMAN-X2.DNA	501	GGGCTGTACT		CTGGTGGTTT	GATGCATGTC	TTTCTGCAAA	550
		560	570	580	590	600	
MOUSE-X2.DNA		CTTAAATGGC					600
HUMAN-X2.DNA	551	CTTAAATGGC			CAGAGGTGTC	CGTAATGGGA	600
		610	620	630	640	650	
MOUSE-X2.DNA		TTTTCTGGGG					650
HUMAN-X2.DNA	601	TTTTCTGGGG				TGGTGGCTAC	650
		660	670	680	690	700	
MOUSE-X2.DNA		AAGTCCTCCT					700
HUMAN-X2.DNA	651	AAGTCCTCCT	TCAAAGAGGC	TAAGATGATG	ATCAGACCCA	AGCACTTTAA	700
		710	720	730	740	750	
MOUSE-X2.DNA		GCCATAA	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • •	• • • • • • • • •		750
HUMAN-X2.DNA	701	GCCATAA	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	750

10	20	. 30	40	50	60
ATCACTCTGT	TCATTCCTCC	AGGTATTCGT	TATCTAATAG	GGCAATTAAT	TCCTTCAGCA
70	80	90	100	110	120
CTTTAGAATA	TGCCTTGTTT	CATATTTTTC	ATAGCTAAAA	AATGCCTTGT	TTCATATTTT
130	140	150	160	170	180
TCATAGCTAA	AAAATGATGT	CTGACGGCTA	GGTTCTTATG	CTACACAGCA	TTTGAAATAA
190	200	210	220	230	240
AGCTGAAAAA	CAATGCATTT	TAAAGGAGTC	CTTTGTTGTT	ATGCTGTTAT	CCAATGAACA
250	260	270	280	290	300
CTTGCAAGCA	ATTAGCARTA	TTGAGAATTA	TACATTAGAT	TTACAATTCT	TTTAATTTCT
310	320	330	340	350	360
ATTGAAACTT	TTTCTATTGC	TTGTATTACT	TGCTGTATTT	AAAAAATAAT	TGTTGGCTGG
370	380	390	400	410	420
GTGTGGTAGC	TCACGCCTGT	AATNCCAGCA	CTTTGGAATG	TCAAGGCAGG	CAGATCACTT
430	440	450	460	470	480
GAGGTCAGGA	GTTTGAGACC	AGCCTGGCCA	AACATGTGAA	ACGCTGTNTN	TATTAAAAAT
490	500	510	520	530	540
ACAAAAATTA	GCCGGGCATG	GTGGNACATG	CCTGTAATCC	TAGNTACTTG	
550	560	570	580	590	600
GCAGGAGAAT	CGCTTGAACC	TGAGAGGAAG	AGGTTGCAGT		TGAGCCACTG
610	620	630	640	650	660
CACTCCAGCA	TGGGTGACAG	AGAAAACTCT	GTCTCAAACA	AAAAAAAA	
670	680	690	700	710	720
CAGTAGGNTG	GATTCTACAC	AAAGTAATCT	GTATTTGGGC		GCACATCTGA
730	740	750	760	770	780
AGGTATATCA	CTCTTTTCAG	GCTATAATTA	TTTGGGTAAT		AGACAAACTT
790	800	810	820	830	840
AATCTATATC	ATTTACTTTG	CARCAGRACA	ACCCTACAGC	ATTTTGGTTC	CCAGACTAAG
850	860	870	880	890	900
GGAACTAATA	TCTATATAAT	TAAACTTGTT	CATTTATCAT		TAAAATI.CTT
910	920	930	940	950	960
GTCATTTAAA	CCGTTTAAAA	ATGTGGTAGC	ATAATGTCAC		
970	980	990	1000	1010	1020
CAATGTAACT	GTGAAGACCA	GGGTTTAAAG	GTAATTCATT		
1030	1040	1050	1060		
ATGTTTGATG	TTGAAAACTG	CTTTAACATG	AA		

3'UTR of hfgl2. The A at position 1 corresponds to position 1354 on the cDNA.

		10	20	30	40	50	
MOUSEPRO.AMI	1	R PG LANGE	SAVLAACR-A	EEHEL WGL	ENASHQAA	ARIBEGSER	50
HUMANPRO.AMI	1	KANNYTH			KERKOV	VRIESREKEE	50
		60	70	80	90	100	
MOUSEPRO.AMI	51	-GSQCI F. LT	LFTLTIQLIR	LGSMEEVL	EVRTUKEAVD	BLKKSCODCE	100
HUMANPRO.AMI	51	EAGE Y VS	LPP LT I OLEK	FSRIFINF	NAIENENOAS	SLKKSCODOF	100
		110	120	130	140	150	
MOUSEPRO.AMI	101	LOADLHRDPG	GNGGN	GAETAE SRI	QELES OVNKL	SSELKNARDO	150
HUMANPRO.AMI	101	LQADD <mark>NG</mark> DPG	RNGLLLPSTG	APGEVGENEV	RELESEVNKL	SSELKNAKDE	150
		160	170	180	190	200	
MOUSEPRO.AMI	151	I QGLQ GRLET	EHLVNMNNIB	NYVD <mark>N</mark> KVANI.	IVVVNSLDGE	JSKCPSOFHM	200
HUMANPRO.AMI	151	INVLHSRUEK	LNLVNMNNIE	NYVDSKVANI	I FVVNSLDGK	JSKCPSOE OI	200
		210	220	230	240	250	
MOUSEPRO.AMI	201	25 <b>€</b> PVOHLIY	KDCSDH:VI	RRSSGA (RVT	PD <mark>HR</mark> NSSFEV	(CDMETMGGG	250
HUMANPRO.AMI	201	<b>DSRPVOHLIY</b>	KDCSIYTAI.	KRSS <b>ET</b> YRVT	PD <b>PK</b> NSSFEV	CDMETMGGG	250
		260	270	280	290	300	
MOUSEPRO.AMI	251	ATVLQARLDG	STNETPD:K	rKAGFGNL <b>D</b> r	SEWLGNDK1H	LLTKSKEMII	300
HUMANPRO.AMI	251	MTVLQARLDG	STNFTPT (C	YKAGEGNI RE	EFWLGNDKIR	LITKSKEMIL	300
		310	320	330	340	350	
MOUSEPRO.AMI		RIDLEDFNGL	TLYALYDOFY	√ANEFLKYRI.	<b>I</b> JNYNGTAG	DALRE SRHYE	350
HUMANPRO.AMI	301	RIDLEDENGV	ELYALYDOFY	√ANEFLKYRL	-WGNYNGTAG	JALRENKHYE	350
		360	370	380	390	400	
MOUSEPRO.AMI		HDLREFTTPL	RONDRYPSGE	JGLYYSSGW.	FLSCLSANLR	SKYYHOKYK -	400
HUMANPRO.AMI	351	HDLKEFTTPL	<b>K</b> DNDRYPSGN	JGLYYSSGWW	FUACLSANLE	SKYYHOKYR -	400
		410	420	430	440	450	
MOUSEPRO.AMI		VRNGI FWGTW	<b>SCINOTO BGG</b>	/KSSFK@AKE	HRPKNEKI*	• • • • • • • • • • • • • • • • • • • •	450
HUMANPRO.AMI	401	VRNGIFWGTV.	egvse ahegg	YKSSFK <b>≥</b> AKE	AIRPKHEKE*		450

		10	20	30	40	50	
MOUSEPRO.AMI	1	MRLPGWLWLS	SAVLAACR-A	VEEHNLTEGL	EDASAQAACP	ARLEGSGRCE	50
HUMANPRO.AMI	1	MKLANWYWLS	SAVLATYGFL	<b>VVANNETEEI</b>	KDERAKDVCP	VRLESRGKCE	50
		60	70	80	90	100	
MOUSEPRO.AMI	51	-GSQCPFQLT	LPTLTIQLPR	QLGSMEEVLK	EVRTLKEAVD	SLKKSCQDCK	100
HUMANPRO.AMI	51	EAGECPYQVS	LPPLTIQLPK	QFSRIEEVFK	EVQNLKEIVN	SLKKSCQDCK	100
		110	120	130	140	150	
MOUSEPRO.AMI	101	LQADDHRDPG	GNGGN	GAETAEDSRV	QELESQVNKL	SSELKNAKDQ	150
HUMANPRO.AMI	101	LQADDNGDPG	RNGLLLPSTG	<b>APGEVGDNRV</b>	RELESEVNKL	SSELKNAKEE	150
•		160	170	180	190	200	
MOUSEPRO.AMI		IQGLQGRLET					200
HUMANPRO.AMI	151	INVLHGRLEK	LNLVNMNNIE	NYVDSKVANL	TEVVNSLDGK	CSKCPSQEQI	200
		210	220	230	240	250	
MOUSEPRO.AMI	201	QSQPVQHLIY	KDCSDHYVLG	RRSSGAYRVT	PDHRNSSFEV	YCDMETMGGG	250
HUMANPRO.AMI	201	QSRPVQHLIY	KDCSDYYAIG	KRSSETYRVT	PDPKNSSFEV	YCDMETMGGG	250
		260	270	280	290	300	
MOUSEPRO.AMI	251	WTVLQARLDG	STNFTREWKD	YKAGFGNLER	EFWLGNDKIH	LLTKSKEMIL	300
HUMANPRO.AMI	251	WTVLQARLDG	STNFTRTWQD	YKAGFGNLRR	EFWLGNDKIH	LLTKSKEMIL	300
		310	320	330	340	350	
MOUSEPRO.AMI	301	RIDLEDFNGL	TLYALYDQFY	VANEFLKYRL	HIGNYNGTAG	DALRFSRHYN	350
HUMANPRO.AMI	301	RIDLEDFNGV	ELYALYDQFY	VANEFLKYRL	HVGNYNGTAG	DALRFNKHYN	350
		360	370	380	390	400	
MOUSEPRO.AMI		HDLRFFTTPD					400
HUMANPRO.AMI	351	HDLKFFTTPD	KDNDRYPSGN	CGLYYSSGWW	FDACLSANLN	GKYYHQKYRG	400
		410	420	430	440	450	
MOUSEPRO.AMI	401	VRNGIFWGTW	PGINQAQPGG	YKSSFKQAKM	MIRPKNFKP*		450
HUMANPRO.AMI	401	VRNGIFWGTW	PGVSEAHPGG	YKSSFKEAKM	MIRPKHFKP*		450

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TURN COIL	1111111	290 KIHLLT	TTT TT 300 KSKEMILR	310	TTTTTT  320 LYALYDQFYVA	TTTT: 330 Heflkyrlh	TTT TTTT 340	350
TURN COIL HELIX SHEET	EFWLGHU	290 KIHLLT	TTT TT 300 KSKEHILR hhhhhhh	TTTTTT 310 IDLEDFNGVE hhhhhhhhhhh	TTTTTT  320 LYALYDQFYVA	TTTT: 330 Meflkyrlh Mhhhh	TTT TTTT 340 VGHYNGTAGD	350
TURN COIL HELIX SHEET TURN	EPWLGHI	290 OKIHLLT hhhhhh	TTT TT 300 KSKEHILR hhhhhhh	TTTTTT 310 IDLEDFNGVE hhhhhhhhhhh	TITTIT  320  LYALYDQFYVA	330 Weflkyrlh Whinhh Ssssssss	TTT TTTT 340 VGHYNGTAGD	350 ALRENKHYN
TURN COIL HELIX SHEET	EPWLGNI HHHh	290 OKIHLLT hhhhhh	300 KSKEMILR Whbhhbhb SSSS	310 IDLEDFNGVE hhhhhhhhh SSa SS:	TITTIT  320  LYALYDQFYVA	330 Weflkyrlh Whinhh Ssssssss	340 VGNYNGTAGD	SECCE 350 ALRENKHYN
TURN COIL HELIX SHEET TURN	EPWLGNI HHHh	290 PKIHLLT hhhhhh SSSSS	300 KSKEMILR hhhHhhhh SSSS	310 310 IDLEDFNGVEI hhhHhhhhhh SSa SSI TTTT	TIITIT  J20 LYALYDQFYVA nhhhhhhhhhh	330 Weflkyrlh Whinhh Ssssssss	340 VGNYNGTAGD	CCCCC 350 ALRENKHYN
TURN COIL HELIX SHEET TURN	EPWLGHE HHHH	290 OKIHLLT hhhhhh SSSSS	300 KSKEMILR John Hohnhoh SSSS	310 IDLEDFNGVE: hhHHhhhhhhlisss ss: TTTT	TITTIT  J20 -YALYDQFYVA hhhhhhhhhhh ssssssssss	330 MEFLKYRLH MhhhhH SSSSSSSSS T	340 VGNYNGTAGD	STORY
TURN COIL HELIX SHEET TURN COIL	EPWLGHE HHHh SSSS TITT	290 OKIHILT hhhhhh SSSSS TT T 360 TTPDKDN	300 KSKEMILR John Hohnhoh SSSS	310 310 IDLEDFNGVEI hhhHhhhhhh SSa SSI TTTT	TITTIT  J20 -YALYDQFYVA hhhhhhhhhhh ssssssssss	330 MEFLKYRLH MhhhhH SSSSSSSSS T	340 VGNYNGTAGD	STORY
TURN COIL HELIX SHEET TURN COIL HELIX	EPWLGHE HHHh SEES TITT	290 PKIHLLT hhhhhh SSSSST TT 360 PTPDKDN	300 KSKEMILR John Hohnhoh SSSS	310 IDLEDFNGVEI hhHHhhhhhhi SSa SSI TTTT  380 GLYYSSGNWF	TTITIT  J20 LYALYDQFYVA hhhhhhhhhhh SSSSSSSSSSSSSSSSSSSSSSSSS	330 MEFLKYRLH MhhhhH SSSSSSSSS T	340 VGNYNGTAGD B TTTTTTTTTT 410 RNGIFWGTWE	STORY
TURN COIL HELIX SHEET TURN COIL HELIX SHEET	EPWLGHE HHHh SSSS TTTT  HDLKFF hhhhhi SSSSS	290 OKIHLLT hhhhhh SSSSS TT T  360 FTPDKDN	300 KSKEMILR JOHNHAMAN SSSS TITT 370 HDRYPSGNO	310 IDLEDFNGVEI hhHHhhhhhhli SSS SS: TITT  380 GLYYSSGWF hh	J20 LYALYDQFYVA TATATATATATATATATATATATATATATATATATAT	330 MEFLKYRLH MhhhhH SSSSBSSB T 400 KYYHQKYRGV	340 VGNYNGTAGD B TTTTTTTTTT 410 RNGIFWGTWE	STORY STATE OF STATE
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN	EPWLGHE HHHh SSSS TTTT  HDLKFF hhhhhi SSSSS	290 OKIHLLT hhhhhh SSSSS TT T  360 FTPDKDN	300 KSKEMILR JOHNHAMAN SSSS TITT 370 HDRYPSGNO	310 IDLEDFNGVEI hhHHhhhhhhi SSa SSI TTTT  380 GLYYSSGNWF	J20 LYALYDQFYVA TATATATATATATATATATATATATATATATATATAT	330 MEFLKYRLH MhhhhH SSSSBSSB T 400 KYYHQKYRGV	340 VGNYNGTAGD  * TTTTTTTTTT  410 TRNGIFWGTWG	STORY STATE OF STATE
TURN COIL HELIX SHEET TURN COIL HELIX SHEET	EPWLGHE HHHh SSSS TTTT  HDLKFF hhhhhi SSSSS	290 OKIHLLT hhhhhh SSSSS TT T  360 FTPDKDN	300 KSKEMILR JOHNHAMAN SSSS TITT 370 HDRYPSGNO	310 IDLEDFNGVEI hhHHhhhhhhli SSS SS: TITT  380 GLYYSSGWF hh	J20 LYALYDQFYVA TATATATATATATATATATATATATATATATATATAT	330 MEFLKYRLH MhhhhH SSSSBSSB T 400 KYYHQKYRGV	340 VGNYNGTAGD  * TTTTTTTTTT  410 TRNGIFWGTWG	STORY STATE OF STATE
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN	EPWLGHE HHHh SSSS TTTT  HDLKFF hhhhhi SSSSS	290 OKIHLLT hhhhhh SSSSS TT T  360 FTPDKDN hh	300 KSKEMILR hhhHhhhh SSSS TTT  370 HDRYPSGNO	310 IDLEDFNGVEI hhHHhhhhhhli SSS SS: TITT  380 GLYYSSGWF hh	J20 LYALYDQFYVA TATATATATATATATATATATATATATATATATATAT	330 MEFLKYRLH MhhhhH SSSSBSSB T 400 KYYHQKYRGV	340 VGNYNGTAGD  * TTTTTTTTTT  410 TRNGIFWGTWG	STORY STATE OF STATE
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN	EFWLGHE HHHH BBBB TTTT  HDLKFFT hhhhhi BBSSSSTTT	290 OKIHILT hhhhhh SSSSS TT T  360 FTPDKDN hh SS	300 KSKEMILR hhhHhhhh SSSS TIT  370 HDRYPSGNO	310 IDLEDFNGVEI hhHHhhhhhhli SSS SS: TITT  380 GLYYSSGWF hh	J20 LYALYDQFYVA TATATATATATATATATATATATATATATATATATAT	330 MEFLKYRLH MhhhhH SSSSBSSB T 400 KYYHQKYRGV	340 VGNYNGTAGD  * TTTTTTTTTT  410 TRNGIFWGTWG	STORY STATE OF STATE
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN COIL	EFWLGHE HHHH BBBB TTTT  HDLKFFT hhhhhi BBSSSSTTT  YKSSFK	290 OKIHLLT hhbbhh SSSSS TT T  360 FTPDKDN hh SS	300 KSKEMILR hhhHhhhh SSSS TTT  370 HDRYPSGNO	310 IDLEDFNGVEI hhHHhhhhhhli SSS SS: TITT  380 GLYYSSGWF hh	J20 LYALYDQFYVA TATATATATATATATATATATATATATATATATATAT	330 MEFLKYRLH MhhhhH SSSSBSSB T 400 KYYHQKYRGV	340 VGNYNGTAGD  * TTTTTTTTTT  410 TRNGIFWGTWG	STORY STATE OF STATE
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN COIL	EFWLGHE HHHHh BBBB TTTT  HDLKFF hhhhhi BBSSSS TTT  YKSSFK	290 OKIHLLT hbbbbb SSSSST TT 360 FTPDKDN hb SS TTTTTT  430 EARTMI	300 KSKEMILR hhhHhhhh SSSS TIT  370 HDRYPSGNO	310 IDLEDFNGVEI hhHHhhhhhhli SSS SS: TITT  380 GLYYSSGWF hh	J20 LYALYDQFYVA TATATATATATATATATATATATATATATATATATAT	330 MEFLKYRLH MhhhhH SSSSBSSB T 400 KYYHQKYRGV	340 VGNYNGTAGD  * TTTTTTTTTT  410 TRNGIFWGTWG	STORY STATE OF STATE
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN COIL HELIX SHEET	EFWLGHE HHHH BBBB TTTT  HDLKFFT hhhhhi BBSSSSTTT  YKSSFK K hh	290 OKIHLLT hhbbhh SSSSS TT T  360 FTPDKDN hh SS TTTTTT  430 EAROMI	300 KSKEMILR hhhHhhhh SSSS TIT  370 HDRYPSGNO	310 IDLEDFNGVEI hhHHhhhhhhli SSS SS: TITT  380 GLYYSSGWF hh	J20 LYALYDQFYVA TATATATATATATATATATATATATATATATATATAT	330 MEFLKYRLH MhhhhH SSSSBSSB T 400 KYYHQKYRGV	340 VGNYNGTAGD  * TTTTTTTTTT  410 TRNGIFWGTWG	STORY STATE OF STATE
TURN COIL HELIX SHEET TURN COIL HELIX SHEET TURN COIL	EFWLGHE HHHHh HDLKFF hhhhhi SSSS TTT  YKSSFK K hh TTITTT	290 OKIHLLT hhbbhh SSSSS TT T  360 FTPDKDN hh SS TTTTTT  430 EAROMI	300 KSKEMILR hhhHhhhh SSSS TIT  370 HDRYPSGNO	310 IDLEDFNGVEI hhHHhhhhhhli SSS SS: TITT  380 GLYYSSGWF hh	J20 LYALYDQFYVA TATATATATATATATATATATATATATATATATATAT	330 MEFLKYRLH MhhhhH SSSSBSSB T 400 KYYHQKYRGV	340 VGNYNGTAGD  * TTTTTTTTTT  410 TRNGIFWGTWG	STORY STATE OF STATE

### FIGURE 8A

W0	_	10	20	30	40	50	
MOUSEPRO.DNA		TCGGTTTGGA					50
HUMANPRO.DNA	1	TAGGGTTGGA				TACAGTCATG	50
MOUSEPRO.DNA	E 1	60	70	80	90	100	
HUMANPRO, DNA		AGAGTGCGGT					100
HOLLING ROLDINA	31	GAAGTGTAAA 110					100
MOUSEPRO.DNA	101		120	130	140	150	
HUMANPRO. DNA		CACACATTTC					150
HOTANE NO. DNA	101	TA-AAATTAA					150
MOUSEPRO.DNA	151	160	170	180	190	200	
HUMANPRO.DNA		GAAAAAAAAT					200
HUMANPRO. DNA	151	ATAAATATGA					· 200
MOUSEPRO.DNA	201	210	220	230	240	250	
HUMANPRO.DNA		CAGCAAAGCC					250
HOTANERO. DIA	201	TAGATTTT 260					250
MOUSEPRO.DNA	251	CATTCCAGAC	270 TTCTCACATA	280	290	300	200
HUMANPRO.DNA		AAAACCC					300
		310	320	330	340		300
MOUSEPRO.DNA	301	AATTTGAA				350	250
HUMANPRO. DNA		CAAATTAAAA					350
	301	360	370	380	390		350
MOUSEPRO.DNA	351	AAAGTCTT				400	400
HUMANPRO. DNA		CTTCAGCCTC					400 400
		410	420	430	440	450	400
MOUSEPRO.DNA	401	ATGGTGGTAC					450
HUMANPRO.DNA		GTTTTGA-AC					450
		460	470	480	490	500	430
MOUSEPRO.DNA	451	ATCAGGAGTT					500
HUMANPRO.DNA		ACCAGCG					500
		510	520	530	540	550	300
MOUSEPRO.DNA	501	TAAGAGATAG	ATTACAGAGT	GCCTTTAACT	AGTACAGAGA		550
HUMANPRO.DNA		CTACCTGCAG					550
		560	570	580	590	600	
MOUSEPRO.DNA	551	GTTTATCTGT	GTCAGTTACG	CTGAAATAAT	TTTTAAGTAA	TAAAATCCCT	600
HUMANPRO.DNA	551	GACAGACACT	GGCATA-G	CTCAAA-GAT	T.CACATTTGA	GCAGC	600
		610	620	630	640	650	
MOUSEPRO.DNA		TTTAATAAGA					650
HUMANPRO.DNA	601	TGTGGAAGAT	GACAGTACAA	TTACCAAAAT	GT-CGAAGGG	CAAAGGAG	650
		660	670	680	690	700	•
MOUSEPRO.DNA		ACCCCCAGCT					700
HUMANPRO.DNA	651	GCAGCT		-TGATGA	AAGACAATTA	TGTCCTTT	700
		710	720	730	740	750	•
MOUSEPRO.DNA		TGTGTGAGTG					750
HUMANPRO.DNA	701	TAAATGGGTC					750
MOUGEBRO SVI	25.	760	770	780	790	800	
MOUSEPRO. DNA		CTGCACAGTC					800
HUMANPRO.DNA	121	CAAAGGAAT-					800
MOUSEPRO.DNA	0.01	810	820	830	840	850	
HUMANPRO.DNA		TTACAAACAG					850
HOPMIT NO. DINA	901	TTTCAAGTAG					850
		860	870	880	890	900	

### FIGURE 8B

MOUSEPRO.DNA	851	TTTGTTCTGA	TTAGGGGCAA	TTTTAAGTAC	TTAAGAGTTC	ACACAAAGTC	900
HUMANPRO.DNA	851	TTTGTTACAC	TTAGAAACTT	CTAAAAGTGC	TTAAGATTTC	ACCTGAAAGT	900
		910	920	930	940	950	300
MOUSEPRO.DNA	901	TAGCCTTCAA	AAAGAAAACA	GGTTCCCAAA	CTA	-GGGAGGAAA	950
HUMANPRO.DNA	901	CCAACAT-GA	AGAAAATACA	GGCTCCCCAA	TGCCCCATTC	TAAGAAGAAA	950
		960	970	980	990	1000	330
MOUSEPRO.DNA	951	CAGAATCATT	TCCATTTTGG	TGACATTTA-	GTGGGAAGAA		1000
HUMANPRO.DNA	951	AAGGACCATT		TAACGTTTCT			1000
		1010	1020	1030	1040	1050	1000
MOUSE PRO. DNA	1001	ATTTAGACGT	TCCAACTCTT	TCCCCACTAG	TGG		1050
HUMANPRO.DNA	1001	AACTAGCTCT	TACTTTTTAT		TGTTTTTCCA		1050
		1060	1070	1080	1090	1100	1030
MOUSEPRO.DNA	1051	ATAATATGGT	ATCTTTTGGG	CACTGGTATT	ACAA-CTGTT		1100
HUMANPRO.DNA	1051	GTATAATTAT		CG-TAGTATA			1100
		1110	1120	1130	1140	1150	2100
MOUSEPRO.DNA	1101	AAGACTTTCC	TTGTGCTTTA	CTAAAAAC-C	CA-GACGGTG	AATCTTGAAT	1150
HUMANPRO.DNA		AAGACTTTTC		TAAAATACAT			1150
•	•	1160	1170	1180	1190	1200	1150
MOUSE PRO. DNA	1151	ACAATGCGTG	GCACCCACGG	CAGGCATTCT	ATTGTGCATA		1200
HUMANPRO.DNA	1151	TGGCTGTGTA	CATTTGACTA	TAATAATTTC	AATGCATATT	ATTTCTATTG	1200
		1210	1220	1230	1240	1250	2200
MOUSEPRO.DNA	1201	ACAGGAGATG	ACAGCATTTG	GCTGGCTGCG	CTTGCTGAGG	ACCCTCTCCT	1250
HUMANPRO.DNA	1201	AGAGTAAGTT	ACAGTTTTTG	GCAAACTGCG	TTTGATGAGG	GCTATCTCCT	1250
		1260	1270	1280	1290	1300	
MOUSEPRO.DNA	1251	CCTG-TGTG-	GCGTCTGAGA	CT-GTGATGC	AAATGCGCCC	GCCCTTTTCT	1300
HUMANPRO.DNA	1251	CTTCCTGTGC	GTTTCTAAAA	CTTGTGATGC	AAACGCTCCC	ACCCTTTCCT	1300
		1310	1320	1330	1340	1350	
MOUSEPRO.DNA	1301	GGGAACTCAG	AACGCCTGAG	TCAGGCGGCG	GTGGCTATTA	AAGCG	1350
HUMANPRO.DNA	1301	GGGAACACAG	AAAGCCTGAC	TCAGGCCATG	GCCGCTATTA	AAGCAGCTCC	1350
		1360	1370	1380	1390	1400	
MOUSEPRO.DNA	1351	CCTGGTC	AGGCT	GGGCT-GCCG	CACTGCAAGG	ATG	1400
HUMANPRO.DNA	1351	AGCCCTGCGC	ACTCCCTGCT	GGGTGAGCAG	CACTGTAAAG	ATG	1400

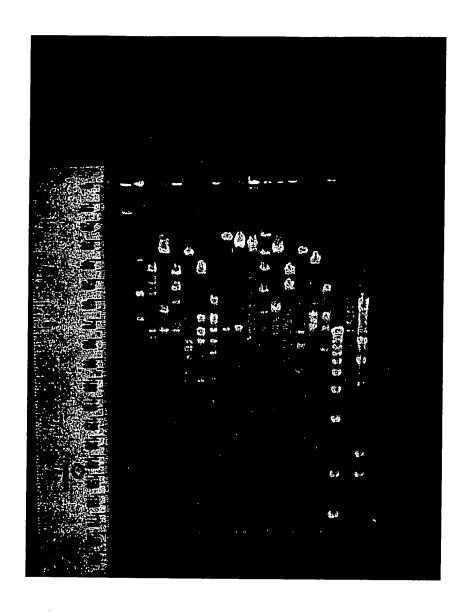
#### FIGURE 9A

10	20	30	40	50
TAGGGTTGGA	AGCCAGGTCTC	CTGAGTATGO	GAGAATAAAT.	ACAGTCATG
60	70	80	90	100
GAAGTGTAAAG	GAGTCTGCCAA	CATTTTGAGA	AATGTGAATAG	GATTTGGCT
110	120	130	140	150
AAAATTAAGG(	GATATACAGA	AAAGTCATAG		
	TC		EA3	•
160	170	180	190	200
AAATATGA <u>GA</u> I	<b>LAGGCTACAGA</b>	GTGTTTTAAC		ΔΔΔCΔΤΤΤΔ
GA 7	Γ <b>λ</b> 1	NF		CAIIIA
210	220	230	240	250
GATTTTTGCCC				
	omio i ono i on	NF IL6	MILLITANAG	CAAAAAAAC
260	270	280	290	200
CCTTTTTAAAC			とうひ これなでなでなれる	300
	DANCHARICII	A I GAGA I G I (	JAHTHIGCHAA	ACAAAIIAA
310	320	330	340	350
AAGGAGGTGG	TTTCTCTAACT	<b>TTDTTDAAGCTGTT</b>	CCTCTTTCCT	CCTTCAGCC
TCF1				
360	370	380	390	400
TCTGAAGAGA	AAGTTAGAAA	ACTATTATCA	TTAATGCTAC	ATGTTTTGAA
		NF_E1		
410	420	430	440	450
			AGGTAGAAGA	
	bHLH			
460		480	490	500
	<del>+</del> · -		GCTACC <u>TGCA</u>	
nonononnno	Onnonogoco.	occ roccaoc	NF	•
510	520	530		550
			GACAGACACT	
TCF1	IGINGCHAG	HORAGI I CAC	GACAGACAC I	GGCH I HGC <u>IC</u>
560	570	580	590	600
TCF1			ATGACAGTACA	ATTACCAAAA
ICFI				
610	E2.			450
610		630		
161CGAAGGG	i	AGCTACTGG	TT <u>TGATGAAA</u>	
	TCF1		NF IL6	
660	- · ·			
			CATTTATATAC	
710				
• * *	AATAGAAAGTA	GCACTTTTT:	TCTCCACTAGT	TTTCTTCTCT
TCF1				
760				
TTTTCAAGTA			GCAATAGTCAG	SAAAGCTGTAC
	TC	F1 bHLH		

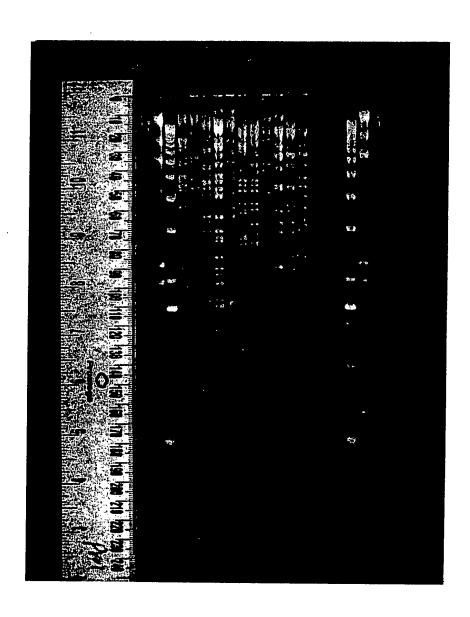
#### FIGURE 9B

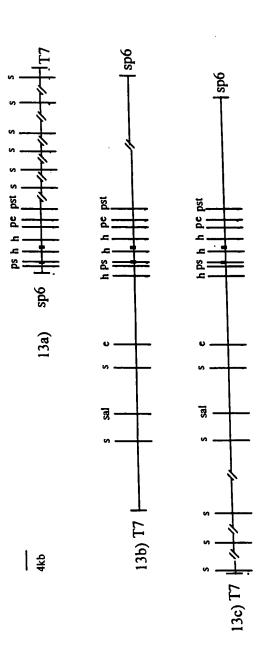
810	820	830	840	850
TTTGTTACACT	TAGAAACTTCTAA	AAGTGCTTA	AGATTT <u>CACC</u>	TGAAACG
		F1	ЬHL	
860	870	880	890	900
CCAACATGAAG	AAAATACAGGCTC	CCCAATGCC	CCATTCTAAG	
910	920		940	950
AGGACCATTTT	CATTTTAGTAACG	TTTCTGTTC	TATAGACAGT	TTGGATA
960	970	980	990	1000
ACTAGCTCTTA	CTTTTTATCTTTA	AAAACTGTT	TTTCCAGTGA	AGTTACG
1010	1020	1030	1040	1050
TATAATTATTT	ACTTCAAGCGTAG	TATACCAAA	TTACTTTAGA	AATGCAA
			NF I	
1060	1070	1080	1090	1100
<b>GACTTTTCTTA</b>	TACTTCATAAAAT	<b>ACATTATGA</b>	AAGTGAATCT	TGTTGGC
		NF II		
1110	1120	1130	1140	1150
TGTGTACATTT	GACTATAATAATT	TCAATGCAT	ATTATTTCTA	TTGAGAG
<b>PHTH</b>				
1160	1170	1180	1190	1200
TAAGTTACAGT	TTTTGGCAAACTG	CGTTTGATO	AGGGCTATCT	CCTCTTC
1210	1220	1230	1240	1250
CTGTGCGTTTC	TAAAACTT <u>GTGAT</u>	<b>GCAA</b> :ACGCT	CCCACCCTTT	'CCTGGGA
	AAE	3S		
1260	1270	1280		1300
ACACAGAAACG	CTGACTCAGGCAC	GTGCCGCTA	TTAAAGCAGC	TCCAGCC
+1	AP 1 bHI	TAT H.	A box	
1310	1320			
CTGCGCACTCC	CTGCTGGGTGAGC	AGCACTGTA	AAG <u>ATG</u>	

### FIGURE 10A



#### FIGURE 10B

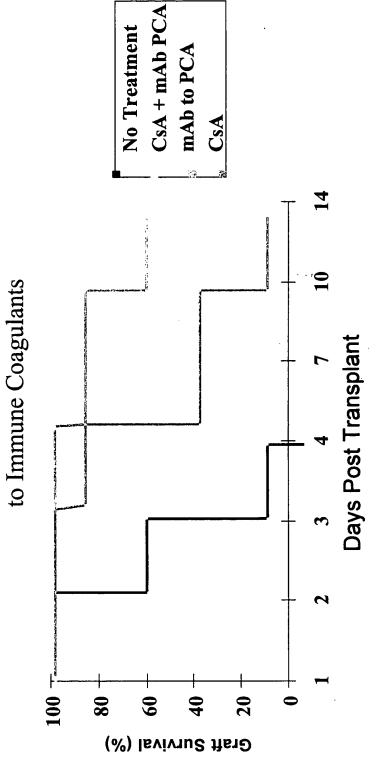


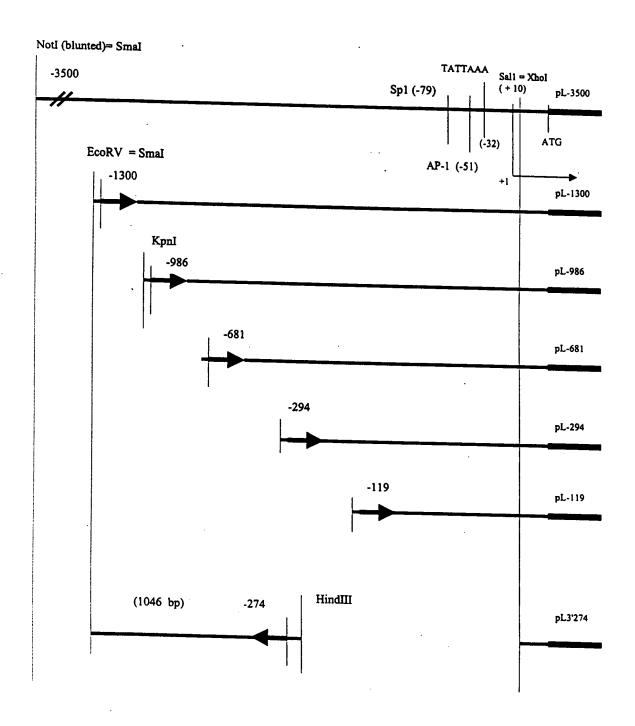


11,

FIGURE 12

Prevention of CsA Graft Rejection by CsA Alone or in Combination with Antibodies





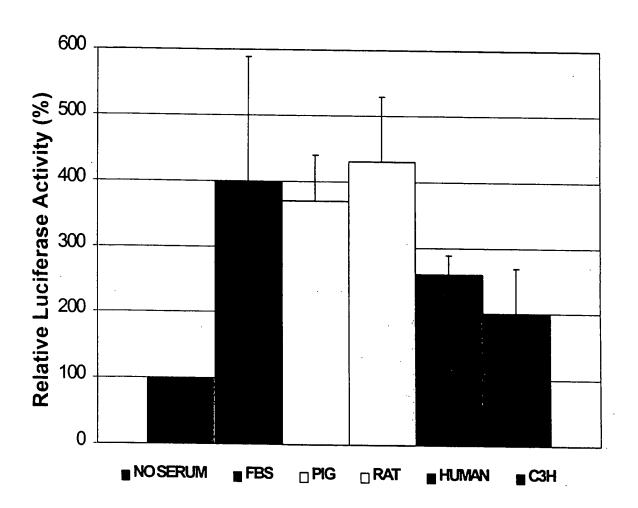
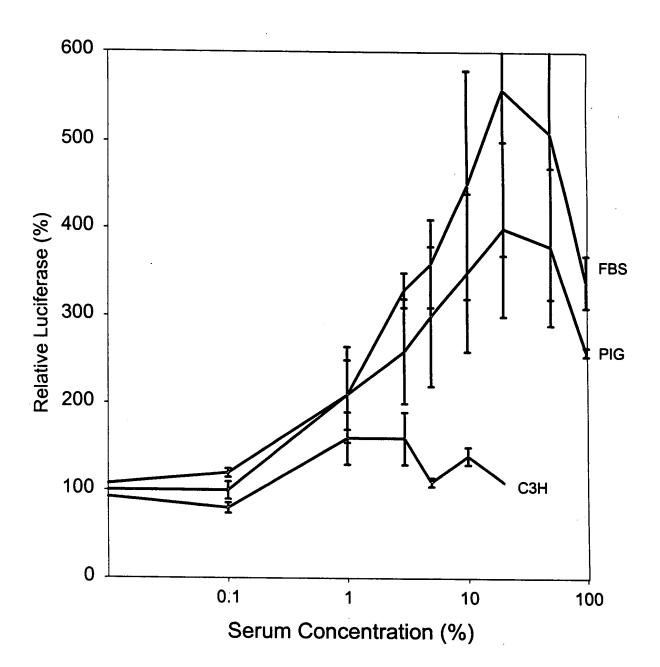


FIGURE 15



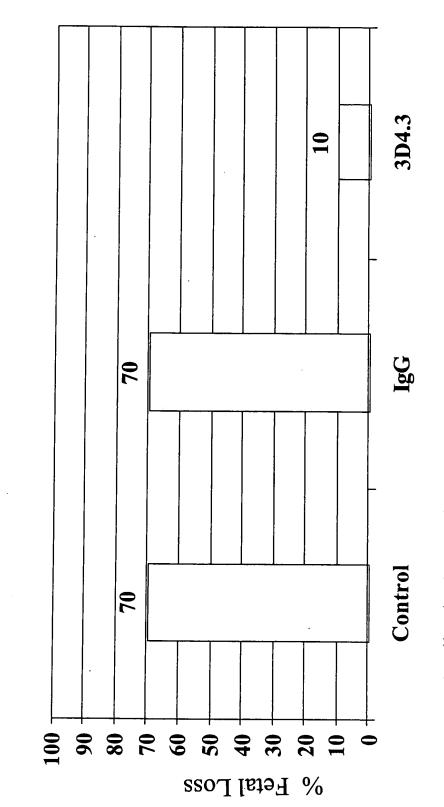
-274 3'del -3.5kbp -1.3kpb -986 bp -681bp -294 bp -119 bp 500 450 400 300 250 100 100 0 % Increase over Serum Free

Figure 16

5'-- CCAAGTATAT AATATGGTAT CTTTTGGGCA CTGGTATTAC AACTGTTTTT -270
TAAACAAAAG ACTTTCCTTG TGCTTTACTA AAAACCCAGA CGGTGAATCT -220
TGAATACAAT GCGTGGCACC CACGGCAGGC ATTCTATTGT GCATAGTTTT -170
GACTGACAGG AGATGACAGC ATTTGGCTGC GTGCGCTTGC TGAGGACCCT -120
CTCCTCCTGT GTGGCGTCTG AGACTGTGAT GCAAATGCGC CCGCCCTTTT -70
CTGGGAACTC AGAANGCCTG AGTCAGGCGG CGGTGGCTAT TAAAGCGCCT -20
GGTCAGGCTG GGCTGCCGCA CTCCAAGG--3'

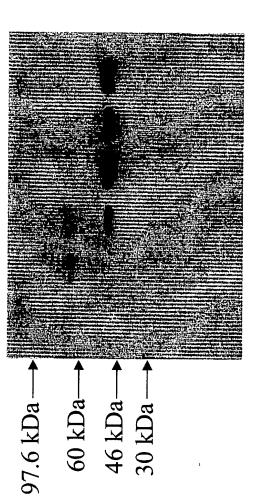
+1

Prevention of Fetal Loss by Monoclonal Antibody 3D4.3 FIGURE 18

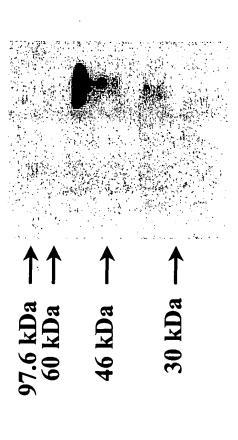


Antibody (10 µg/day I.V. given for 14 days

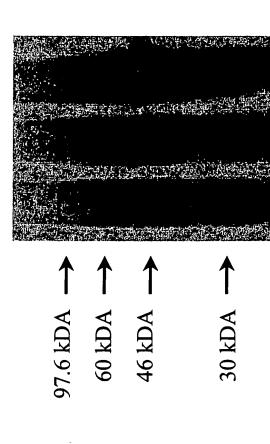
. .



0 24 48 72 96 120 hour postinfection



- The lanes are:
  1. H5cells
  2. H5 + wild type virus
  3. H5 + recombinant
  virus



- The lanes are:
  1. H5cells
  2. H5 + wild type virus
  3. H5 + recombinant
  virus

3

2

97.6 kDa→





The lanes are:

- 1. 125I-Prothrombin (PT)
- 2. PT + RVV + Factor X
  - 3. PT + H5
- 4. PT + H5-RV
- 5. PT + purified protein (3 µg)

2 3 4